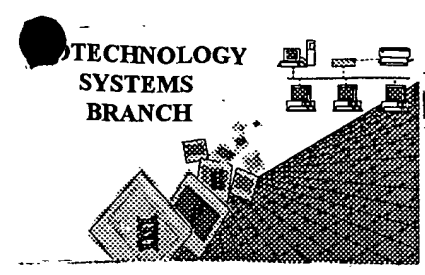


25-490
0429



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/036,918
Source: OIPK
Date Processed by STIC: 4/30/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

101,036,918

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ✓ Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/036,918

DATE: 04/30/2003

TIME: 12:04:00

Input Set : A:\pto.vsk.TXT

Output Set: N:\CRF4\04302003\J036918.raw

3 <110> APPLICANT: Srinivasan, Ananthachari
 4 Erion, Jack L.
 5 Schmidt, Michelle A.
 7 <120> TITLE OF INVENTION: LABELED NEUROTENSIN DERIVATIVES
 9 <130> FILE REFERENCE: 1405Q
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/036,918
 C--> 12 <141> CURRENT FILING DATE: 2003-04-21
 13 <150> PRIOR APPLICATION NUMBER: 60/140,913<151> 1999-06-23
 W--> 15 <150> PRIOR APPLICATION NUMBER: DOCKET NO. 1670-223
 16 <151> PRIOR FILING DATE: 2000-06-21
 18 <160> NUMBER OF SEQ ID NOS: 6
 20 <170> SOFTWARE: PatentIn Ver. 2.0

see pp 1,3-5

Insert a hard return

do not use a docket number for this response.

*Use a
Serial no.*

**Does Not Comply
Corrected Diskette Needed**

ERRORED SEQUENCES

22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 13
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 W--> 28 <221> NAME/KEY: MOD RES<222> (1)<223> Pyroglutamic acid.

this needs an explanation. see p.5 for error explanation

Insert a hard return

Insert a hard return

W--> 31 <400> 1
 W--> 32 Xaa Leu Tyr Glu Asn Lys Pro Arg Arg Bro Tyr Ile Leu
 E--> 33 1 1 5 5 10

35 <210> SEQ ID NO: 2
 36 <211> LENGTH: 6
 37 <212> TYPE: PRT
 38 <213> ORGANISM: Artificial Sequence
 40 <220> FEATURE:
 41 <221> NAME/KEY: MOD_RES
 42 <222> LOCATION: (1)
 43 <223> OTHER INFORMATION: Diethylenetriamine pentaacetic acid (DTPA) is coupled to
 this residue.

misaligned to acid numbering. see item 3

on Error Summary sheet

delete "e"

45 <220> FEATURE:
 46 <221> NAME/KEY: MOD_RES
 47 <222> LOCATION: (1)..(2)
 48 <223> OTHER INFORMATION: These two residues are joined by a pseudo peptide bond.
 50 <220> FEATURE:
 51 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide with a
 pseudopeptide
 52 bond.
 54 <400> SEQUENCE: 2

55 Lys Arg Pro Tyr Ile Leu

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/036,918

DATE: 04/30/2003

TIME: 12:04:00

Input Set : A:\pto.vsk.TXT

Output Set: N:\CRF4\04302003\J036918.raw

E--> 56 1 5 *misaligned amino acid number*
 58 <210> SEQ ID NO: 3
 59 <211> LENGTH: 6
 60 <212> TYPE: PRT
 61 <213> ORGANISM: Artificial Sequence
 63 <220> FEATURE:
 64 <221> NAME/KEY: MOD_RES
 65 <222> LOCATION: (1)
 66 <223> OTHER INFORMATION: Diethylenetriamine pentaacetic acid (DTPA) is coupled to this residue.
 68 <220> FEATURE:
 69 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic peptide.
 71 <400> SEQUENCE: 3
 72 Arg Arg Pro Tyr Ile Leu

E--> 73 1 5 *misaligned nos.*
 75 <210> SEQ ID NO: 4
 76 <211> LENGTH: 8
 77 <212> TYPE: PRT
 78 <213> ORGANISM: Artificial Sequence
 80 <220> FEATURE:
 81 <221> NAME/KEY: MOD_RES
 82 <222> LOCATION: (1)
 83 <223> OTHER INFORMATION: Diethylenetriamine pentaacetic acid (DTPA) is coupled to this residue.
 85 <220> FEATURE:
 86 <221> NAME/KEY: MOD_RES
 87 <222> LOCATION: (1)
 88 <223> OTHER INFORMATION: This residue is piperidinylglycine.
 92 <220> FEATURE:
 93 <221> NAME/KEY: MOD_RES
 94 <222> LOCATION: (3)
 95 <223> OTHER INFORMATION: This residue is (N-amidinopiperidinyl) glycine.
 97 <220> FEATURE:
 98 <221> NAME/KEY: MOD_RES
 99 <222> LOCATION: (7)
 100 <223> OTHER INFORMATION: This residue is t-butylglycine.
 102 <220> FEATURE:
 103 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic peptide.
 105 <400> SEQUENCE: 4

W--> 106 ~~Xaa Pro Xaa Arg Pro Tyr Xaa Leu~~

E--> 107 1 5 *misaligned nos.*
 109 <210> SEQ ID NO: 5
 110 <211> LENGTH: 8
 111 <212> TYPE: PRT
 112 <213> ORGANISM: Artificial Sequence
 114 <220> FEATURE:
 115 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic peptide.
 118 <220> FEATURE:
 119 <221> NAME/KEY: MOD_RES
 120 <222> LOCATION: (1)
 121 <223> OTHER INFORMATION: Diethylenetriamine pentaacetic acid (DTPA) is coupled to this residue.

RAW SEQUENCE LISTING

DATE: 04/30/2003

PATENT APPLICATION: US/10/036,918

TIME: 12:04:00

Input Set : A:\pto.vsk.TXT

Output Set: N:\CRF4\04302003\J036918.raw

123 <220> FEATURE:
124 <221> NAME/KEY: MOD_RES
125 <222> LOCATION: (1)
126 <223> OTHER INFORMATION: This residue is trans-(4-aminomethyl) cyclohexylalanine.
128 <220> FEATURE:
129 <221> NAME/KEY: MOD_RES
130 <222> LOCATION: (3)
131 <223> OTHER INFORMATION: This residue is (N-amidinopiperidinyl) glycine.
134 <220> FEATURE:
135 <221> NAME/KEY: MOD_RES
136 <222> LOCATION: (7)
137 <223> OTHER INFORMATION: This residue is t-butylglycine.
139 <400> SEQUENCE: 5

W--> 140 Xaa Pro Xaa Arg Pro Tyr Xaa Leu
E--> 141 1 5 *misaligned nos.*

143 <210> SEQ ID NO: 6
144 <211> LENGTH: 8
145 <212> TYPE: PRT
146 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:
149 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide.
151 <220> FEATURE:
152 <221> NAME/KEY: MOD_RES
153 <222> LOCATION: (1)
154 <223> OTHER INFORMATION: Diethylenetriamine pentaacetic acid (DTPA) is coupled to
this residue.
156 <220> FEATURE:
157 <221> NAME/KEY: MOD_RES
158 <222> LOCATION: (1)
159 <223> OTHER INFORMATION: This residue is piperidinylalanine.
161 <220> FEATURE:
162 <221> NAME/KEY: MOD_RES
163 <222> LOCATION: (3)
164 <223> OTHER INFORMATION: This residue is (N-amidinopiperidinyl) glycine.
167 <220> FEATURE:
168 <221> NAME/KEY: MOD_RES
169 <222> LOCATION: (7)
170 <223> OTHER INFORMATION: This residue is t-butylglycine.
172 <400> SEQUENCE: 6

W--> 173 Xaa Pro Xaa Arg Pro Tyr Xaa Leu
E--> 174 1 5 *misaligned nos.*

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/036,918

DATE: 04/30/2003
TIME: 12:04:02

Input Set : A:\pto.vsk.TXT
Output Set: N:\CRF4\04302003\J036918.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 51

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:1

error explanation

VARIABLE LOCATION SUMMARY

DATE: 04/30/2003

PATENT APPLICATION: US/10/036,918

TIME: 12:04:02

Input Set : A:\pto.vsk.TXT

Output Set: N:\CRF4\04302003\J036918.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:1; Xaa Pos. 1Seq#:4; Xaa Pos. 1, 3, 7Seq#:5; Xaa Pos. 1, 3, 7Seq#:6; Xaa Pos. 1, 3, 7

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/036,918

DATE: 04/30/2003

TIME: 12:04:02

Input Set : A:\pto.vsk.TXT

Output Set: N:\CRF4\04302003\J036918.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:15 M:289 W: Identifier Missing or Out-Of-Order, <150> PRIOR APP FILING DATE
L:28 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:31 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:31 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:31
L:32 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:1
L:32 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:33 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:56 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:73 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
M:332 Repeated in SeqNo=4
L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
M:332 Repeated in SeqNo=5
L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
M:332 Repeated in SeqNo=6